

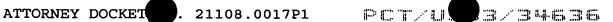
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<110> University of Rochester

Chang, Chawnshang

<120> Hydroxyflutamide Induced Pathways Related to Androgen Receptor Negative Prostate Cancer Cells

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<151> 2002-10-31
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		agactgctcc				660
		ggccccagag				720
		cctgtggagc				780
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Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val Arg
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Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr Leu
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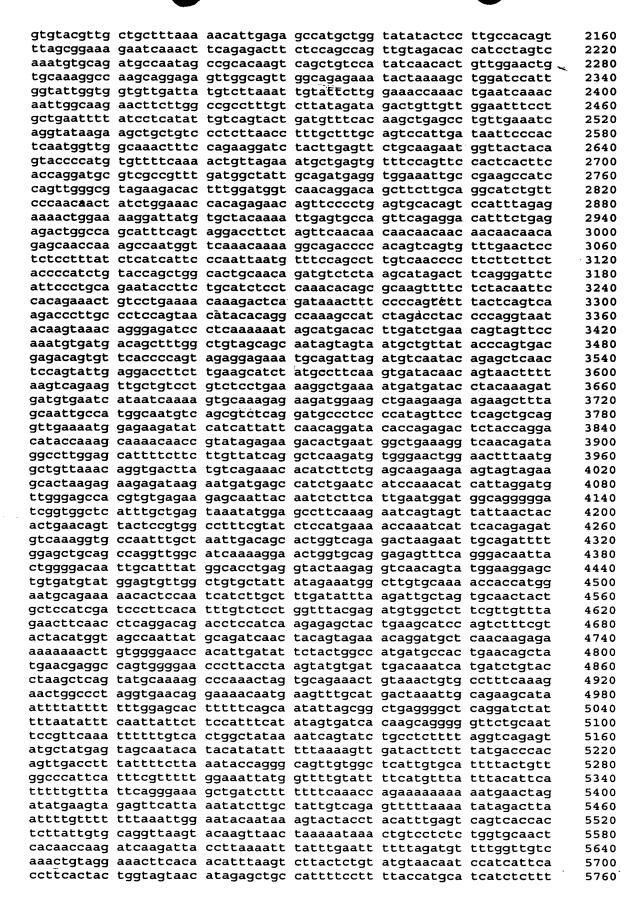
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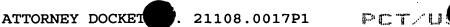
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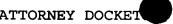




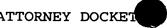
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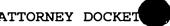
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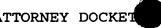


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<213> Artificial Sequence

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<sup>&</sup>lt;223> Description of Artificial Sequence:/note = synthetic construct



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<213> Artificial Sequence

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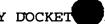
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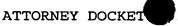
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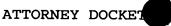
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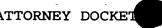
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acatatatca aagtgagaaa atgcctcaat tcacatagat ttcttctctt tagtataatt
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gacctacttt ggtagtggaa tagtgaatac ttactataat ttgacttgaa tatgtagctc
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atcotttaca ccaactocta attttaaata atttctacto tgtottaaat gagaagtact
                                                                    2040
tggttttttt tttcttaaat atgtatatga catttaaatg taacttatta ttttttttga
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gaccgagtct tgctctgtta cccaggctgg agtgcagtgg gtgatcttgg ctcactgcaa
                                                                    2160
getetgeect eccegggtte geaceattet cetgeeteag ceteceaatt agettggeet
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acagtcatct gccaccacac ctggctaatt ttttgtactt ttagtagaga cagggtttca
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ccgtgttagc caggatggtc tcgatctcct gacctcgtga tccgcccacc tcggcctccc
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<210> 22
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- <211> 491
- <212> PRT
- <213> Artificial Sequence

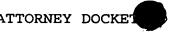


<223> Description of Artificial Sequence:/note = synthetic construct

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Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arq Pro Lys Asn Gly
                            440
Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys
                        455
Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln
                    470
                                        475
Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro
                485
<210> 23
<211> 1599
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence:/note =
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ctccacaagc gtggtgaata catcaagacc tggaggccac ggtacttcct gctgaagagc
                                                                       180
gaeggeteet teattgggta caaggagagg ceegaggeee etgateagae tetaceeeee
                                                                       240
ttaaacaact tctccgtagc agaatgccag ctgatgaaga ccgagaggcc gcgacccaac
                                                                       300
acctttgtca tacgctgcct gcagtggacc acagtcatcg agaggacctt ccacgtggat
                                                                       360
tetecagaeg agaggagga gtggatgegg gecatecaga tggtegecaa cageeteaag
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cagegggccc caggegagga ccccatggac tacaagtgtg gctcccccag tgactcctcc
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gatgaagtcg ctcacacagt caccgagagc cgggtcctcc agaacaccag gcacccgttc
                                                                       720
ctcactgcgc tgaagtatgc cttccagacc cacgaccgcc tgtgctttgt gatggagtat
                                                                       780
gccaacgggg gtgagctgtt cttccacctg tcccqqqaqc gtgtcttcac aqaqqaqcqq
                                                                       840
geceggitti atggtgeaga gattgteteg getettgagt acttgeacte gegggaegtg
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gtatacegeg acateaaget ggaaaacete atgetggaca aagatggeea cateaagate
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                                                                      1080
gactggtggg ggctgggtgt ggtcatgtac gagatgatgt gcggccgcct gcccttctac
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aaccaggacc acgagegect ettegagete atceteatgg aagagateeg etteeegege
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acgeteagee eegaggeeaa gteeetgett getgggetge ttaagaagga eeceaageag
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cagttetect acteggeeag cateegeqaq tqaqeaqtet qeecacqeaq aqqaeqeaq
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<211> 481
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct
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Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Ser Asp
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Gly Ser Phe Ile Gly Tyr Lys Glu Arg Pro Glu Ala Pro Asp Gln Thr 40 Leu Pro Pro Leu Asn Asn Phe Ser Val Ala Glu Cys Gln Leu Met Lys 55 60 Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile Arg Cys Leu Gln Trp 75 Thr Thr Val Ile Glu Arg Thr Phe His Val Asp Ser Pro Asp Glu Arg 90 Glu Glu Trp Met Arg Ala Ile Gln Met Val Ala Asn Ser Leu Lys Gln 105 Arg Ala Pro Gly Glu Asp Pro Met Asp Tyr Lys Cys Gly Ser Pro Ser 120 125 Asp Ser Ser Thr Thr Glu Glu Met Glu Val Ala Val Ser Lys Ala Arq 135 140 Ala Lys Val Thr Met Asn Asp Phe Asp Tyr Leu Lys Leu Gly Lys 150 155 Gly Thr Phe Gly Lys Val Ile Leu Val Arg Glu Lys Ala Thr Gly Arg 170 Tyr Tyr Ala Met Lys Ile Leu Arg Lys Glu Val Ile Ile Ala Lys Asp 180 185 Glu Val Ala His Thr Val Thr Glu Ser Arg Val Leu Gln Asn Thr Arg 200 His Pro Phe Leu Thr Ala Leu Lys Tyr Ala Phe Gln Thr His Asp Arg 215 Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His 230 235 Leu Ser Arg Glu Arg Val Phe Thr Glu Glu Arg Ala Arg Phe Tyr Gly 245 250 Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Ser Arg Asp Val Val 260 265 Tyr Arg Asp Ile Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His 280 Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Ser Asp Gly 295 300 Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu 310 315 Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu 325 330 Gly Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn 345 Gln Asp His Glu Arg Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg 360 Phe Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ala Gly Leu 375 380 Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Pro Ser Asp Ala 390 395 Lys Glu Val Met Glu His Arg Phe Phe Leu Ser Ile Asn Trp Gln Asp 405 410 Val Val Gln Lys Lys Leu Leu Pro Pro Phe Lys Pro Gln Val Thr Ser 425 Glu Val Asp Thr Arg Tyr Phe Asp Asp Glu Phe Thr Ala Gln Ser Ile 440 Thr Ile Thr Pro Pro Asp Arg Tyr Asp Ser Leu Gly Leu Leu Glu Leu 455 460 Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg 465 Glu

<210> 25 <211> 1547

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ATTORNEY DOCKET
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<212> DNA
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:/note = synthetic construct

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aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct
                                                                       240
ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga
                                                                       300
atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat
                                                                       360
                                                                       420
gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac
aacccatcat aaaagaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg
                                                                       480
cacttttggg aaagttattt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa
                                                                       540
gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag
                                                                       600
cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac
                                                                       660
aaaagaccgt ttgtgttttg tgatggaata tgttaatggg ggcgagctgt ttttccattt
                                                                       720
gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc
                                                                       780
tgccttggac tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct
                                                                       840
aatgctggac aaagatggcc acataaaaat tacagatttt ggactttgca aagaagggat
                                                                       900
cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt
                                                                       960
gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta
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tgaaatgatg tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt
                                                                      1080
aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct
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ttcagggctc ttgataaagg atccaaataa acgccttggt ggaggaccag atgatgcaaa
                                                                      1200
agaaattatg agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa
                                                                      1260
gcttgtacct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga
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agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggtat
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ggactgcatg gacaatgaga ggcggccgca tttccctcaa ttttcctact ctgcaagtgg
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acgagaataa gtctctttca ttctgctact tcactgtcat cttcaattta ttactgaaaa
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<210> 26
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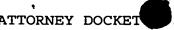
<211> 479

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:/note = synthetic construct

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Gly Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
Met Asn Asp Phe Asp Tyr Leu Lys Leu Cly Lys Gly Thr Phe Gly
                    150
                                        155
Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met
                                    170
Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
                                185
Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
                            200
Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
                        215
                                            220
Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
                    230
                                        235
Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
                245
                                    250
Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
            260
                               ~ 265
                                                    270
Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
                                                285
        275
                            280
Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
                        295
                                            300
Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
                    310
                                        315
Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
                325
                                    330
Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
                                345
Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
                            360
Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
                        375
                                            380
Pro Asn Lys Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
                    390
                                        395
Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
                405
                                    410
Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
            420
                                425
                                                    430
Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
                            440
        435
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Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
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<210> 27
<211> 2277
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence:/note =
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                                                                       120
tgcgagaagg ggaggaggag ccggccgcc gccgccgcc cggggatggt gaggaggcgg
                                                                       180
egetgegtga geecagttag geettegete gggeeegeeg eeagetetee etteeteege
                                                                       240
tegetegete ecceptices teteettees tgeegeegee geegeegees teccateace
                                                                       300
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tcctccccgg gctcccgcag ccataagtag ctgagaagga gaaagacaag aaaaagaaca



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ccaccagcct gataaactga tccaccaaga gacattcccg ccattatgaa tgaagtagcg
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                                                                       540
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                                                                       720
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agaacatttc atgtggagac tccagaggag cgggaagaat ggacaaaagc tatccaaact
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accatgaatg aatttgaata ccttaagcta ctgggaaaag gcacttttgg aaaggtcatt
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eggeatecat tettaacage tttaaagtat teettteaga cacaegateg ettgtgtttt
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tetgaagace gggegegttt ttatgggget gagattgttt cagegetgga ttacetgeat
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tcagagaaga atgtggtgta cagagatttg aagctggaaa atcttatgct ggataaagac
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agaactttct atattatctg aattacaaac tgtgtttgta ttacgattta gatgaatttc
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agaatatgca ccaaaactgt ttactttaga attaattaag gcattcaata tcagctatag
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<210> 28
<211> 480
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:/note = synthetic construct

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- - - ----

Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Gln His Lys Phe Phe Ala Gly Ile Val Trp Gln Asp Val Tyr Gly Lys Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Asp Cys Val Asp Asn Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala